REMARKS

Amendments to the Claims

In the present amendment, Applicants have amended claim 11, added claims 13-16, and cancelled claims 1-10 and 12 without prejudice or disclaimer. Accordingly, following entry of the present amendment, claims 11 and 13-16 are pending.

Claim 11 has been amended to recite a "method for producing optically active cyanohydrin comprising (a) obtaining a modified S-hydroxynitrile lyase, wherein the modified S-hydroxynitrile lyase comprises an amino acid sequence having at least one amino acid substitution in the helix D3 region from position 163 to 174 of SEQ ID NO:2; (b) adding the modified S-hydroxynitrile lyase to a carbonyl compound and cyanide; and (c) producing optically active cyanohydrin." Support for the phrase "obtaining a modified S-hydroxynitrile lyase, wherein the modified S-hydroxynitrile lyase comprises an amino acid sequence having at least one amino acid substitution in the helix D3 region from position 163 to 174 of SEQ ID NO:2" is found in the specification, for example, at least at paragraphs [0009] and [0010]. Support for the phrase "adding the modified S-hydroxynitrile lyase to a carbonyl compound and cyanide" is found in the specification, for example ,at least at paragraph [0017]. Support for the phrase "producing optically active cyanohydrin" is found in the specification, for example, at least at paragraph [0017].

Claim 13 indicates that "the modified S-hydroxynitrile lyase comprises an amino acid sequence having an amino acid substitution at position 165 and/or position 173 of SEQ ID NO: 2." Support is found in the specification, for example, at least at paragraph [0034].

Claim 14 indicates that that "the modified S-hydroxynitrile lyase comprises the amino acid sequence of SEQ ID NO: 8." Support is found in the specification, for example, at least at paragraph [0034].

Claim 15 indicates that "the modified S-hydroxynitrile lyase comprises the amino acid sequence of SEQ ID NO: 16." Support is found in the specification, for example, at least at paragraph [0034].

Claim 16 indicates that "the modified S-hydroxynitrile lyase comprises the amino acid sequence of SEQ ID NO: 32." Support is found in the specification, for example, at least at paragraph [0034].

Accordingly, the claims are fully supported and no new matter has been added. Following entry of the present amendment, claims 11 and 13-16 are pending.

Elections/Restrictions

In the Office Action, a thirty-three way restriction requirement of claims 1-12 was made under 35 USC §§ 121 and 372 as follows:

> **Group I** - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region of amino acid between 15 and 28 of SEQ ID NO: 2 or at position 21 of SEQ ID NO: 2."
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> **Group II** - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the beta- sheet 2 region of amino acid between 32 and 36 of SEQ ID NO: 2."
>
> **Group III** - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 163 of SEQ ID NO: 2."
>
> **Group IV** - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 165 of SEQ ID NO: 2."

Group V - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 169 of SEQ ID NO: 2."

Group VI - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 172 of SEQ ID NO: 2."

Group VII - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 173 of SEQ ID NO: 2."

Group VIII - Claims 1-7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 174 of SEQ ID NO: 2."

Group IX - Claims 1-3 and 7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region of amino acid between 15 and 28 of SEQ ID NO: 4."

Group X - Claims 1-3 and 7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the beta- sheet 2 region of amino acid between 32 and 36 of SEQ ID NO: 4."

Group XI - Claims 1-3 and 7 (in part) allegedly "drawn to a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 4."

Group XII - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region of amino acid between 15 and 28 of SEQ ID NO: 2 or at position 21 of SEQ ID NO: 2."

Group XIII - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the beta sheet 2 region of amino acid between 32 and 36 of SEQ ID NO: 2."

Group XIV - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 163 of SEQ ID NO: 2."

Group XV - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 165 of SEQ ID NO: 2."

Group XVI - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 169 of SEQ ID NO: 2."

Group XVII - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 172 of SEQ ID NO: 2."

Group XVIII - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 173 of SEQ ID NO: 2."

Group XIX - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 174 of SEQ ID NO: 2."

Group XX - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region of amino acid between 15 and 28 of SEQ ID NO: 4."

Group XXI - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the beta-sheet 2 region of amino acid between 32 and 36 of SEQ ID NO: 4."

Group XXII - Claims 8 and 9-10 (in part) allegedly "drawn to a DNA molecule encoding a modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region of amino acid between 162 and 173 of SEQ ID NO: 4."

Group XXIII - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region of amino acid between 15 and 28 of SEQ ID NO: 2 or at position 21 of SEQ ID NO: 2."

Group XXIV - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which

is obtained by modifying at least one amino acid in the beta-sheet 2 region of amino acid between 32 and 36 of SEQ ID NO: 2."

Group XXV - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 163 of SEQ ID NO: 2."

Group XXVI - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 165 of SEQ ID NO: 2."

Group XXVII - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 169 of SEQ ID NO: 2."

Group XXVIII - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 172 of SEQ ID NO: 2."

Group XXIX - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 173 of SEQ ID NO: 2."

Group XXX - Claim 11 (in part) allegedly "drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 162 and 173 of SEQ ID NO: 2 or at position 174 of SEQ ID NO: 2."

Group XXXI - Claim 12 (in part) allegedly "drawn to a method for improving stability of modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix A region."

Group XXXII - Claim 12 (in part) allegedly "drawn to a method for improving stability of modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the beta-sheet 2 region."

Group XXXIII - Claim 12 (in part) allegedly "drawn to a method for improving stability of modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region."

At page 8, the Office further required an election from the following inventions (A) - (L) under 35 U.S.C. 121 and 372:

(A). Protein of SEQ ID NO: 6 or a nucleic acid encoding SEQ ID NO: 6.

(B). Protein of SEQ ID NO: 8 or a nucleic acid encoding SEQ ID NO: 8.

(C). Protein of SEQ ID NO: 16 or a nucleic acid encoding SEQ ID NO: 16.

(D). Protein of SEQ ID NO: 20 or a nucleic acid encoding SEQ ID NO: 20.

(E). Protein of SEQ ID NO: 22 or a nucleic acid encoding SEQ ID NO: 22.

(F). Protein of SEQ ID NO: 24 or a nucleic acid encoding SEQ ID NO: 24.

(G). Protein of SEQ ID NO: 28 or a nucleic acid encoding SEQ ID NO: 28.

(H). Protein of SEQ ID NO: 32 or a nucleic acid encoding SEQ ID NO: 32.

(I). Protein of SEQ ID NO: 36 or a nucleic acid encoding SEQ ID NO: 36.

(J). Protein of SEQ ID NO: 40 or a nucleic acid encoding SEQ ID NO: 40.

(K). Protein of SEQ ID NO: 42 or a nucleic acid encoding SEQ ID NO: 42.

(L). Protein of SEQ ID NO: 44 or a nucleic acid encoding SEQ ID NO: 44.

At the outset, Applicants respectfully note that the helix D3 region of SEQ ID NO: 2 is "is equivalent to the region between amino acids 163 and 174." Specification at paragraph [0024]. However, Groups XXV – XXX indicate that the helix D3 region is between amino acids "162 and 173 of SEQ ID NO: 2." Action at pages 6-7. Applicants respectfully suggest that Groups XXV – XXX should indicate that the D3 region of SEQ ID NO: 2 is between amino acids 163 and 174. Applicants respectfully request clarification and approval from the Examiner that Groups XXV – XXX are drawn to a method for producing optically active cyanohydrin by using the modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 163 and 174 of SEQ ID NO: 2 . . . ."

In the present Action, the Examiner urged that the "inventions listed as Groups I-XXXIII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding technical features." Action at page 8-9.

The Examiner stated that the "polypeptide of SEQ ID NO: 2 or 4 having HNL activity . . . are known in the art, i.e.[,] 100% identical" to "UniProt Accession No. P52705 for SEQ ID NO: 2." *Id.* at page 9. The Examiner concluded that "a modified HNL based on SEQ ID NO: 2 or 4 does not make a contribution over the prior art." *Id.* The Examiner also stated that the "methods of Groups XXIII-XXXIII do not have any unity of invention with each other as each method[] comprises unrelated steps, and use[s] different products, and produce[s] different effects." *Id.*

Regarding Groups A-L, the Examiner stated that the "proteins of Group (A)-(L) are unrelated." Action at page 9. Specifically, the Examiner alleged that those proteins "do not have [a] special technical feature among each other because they all represent structurally different polypeptides and polynucleotides encoding them." *Id.* at page 10.

Applicants respectfully disagree.

As a preliminary matter, as noted above, Applicants have amended claim 11, added claims 13-16, and cancelled claims 1-10 and 12. Applicants respectfully submit that:

- Group XXVI encompasses claims 11, 13, 14, and 16;
- Group XXIX encompasses claims 11, 13, 15, and 16;
- Group B encompasses claims 11, 13, and 14; and
- Group C encompasses claims 11, 13, and 15; and
- Group H encompasses claims 11, 13, and 16.

Applicants assert that it would be eminently feasible for the Examiner to search and examine at least Groups XXVI and XXIX and Groups B, C, and H together.[1]

[1] Applicants note that the Examiner has not provided any class or subclass information for any of the restricted groups.

First, Groups XXVI and XXIX cover overlapping subject matter. For example, a "modified S-hydroxynitrile lyase, which is obtained by modifying at least one amino acid in the helix D3 region of amino acid between 16[3] and 17[4] of SEQ ID NO: 2" is recited in both Groups XXVI and XXIX. Accordingly, the methods of Groups XXVI and XXIX do have unity of invention with each other because they can comprise the identical modified S-hydroxynitrile lyase.

Second, Groups B, C, and H share a special technical. Specifically, the modified S-hydroxynitrile lyases of those Groups have improved stability and heat tolerance compared to the wild-type S-hydroxynitrile lyase encoded by SEQ ID NO: 2. *See e.g.*, paragraph [0034] and Examples 6, 8, and 16-19. Furthermore, searching and examining Groups B, C, and H together poses no additional burden on the Examiner because of their relationship. For example;

- Group H includes the amino acid substitutions to SEQ ID NO: 2 that are present in Group B and Group C;
- SEQ ID NO: 8 of claim 14 (Group B) comprises substitution of amino acid 165 (glycine) of SEQ ID NO: 2 to glutamic acid;
- SEQ ID NO: 16 of claim 15 (Group C) comprises substitution of amino acid 173 (valine) of SEQ ID NO: 2 to leucine; and
- SEQ ID NO: 32 of claim 16 (Group H) comprises substitution of amino acid 165 (glycine) of SEQ ID NO: 2 to glutamic acid and substitution of amino acid 173 (valine) of SEQ ID NO: 2 to leucine.

See specification at paragraph [0034]. Thus, SEQ ID NO: 8 and SEQ ID NO: 16, each, only differ at one amino acid from SEQ ID NO: 32. Thus, the search and examination of Groups B,

C, and H together poses no additional burden on the Examiner compared to search and examination of Group H alone.

Based on the above, Applicants respectfully request reconsideration and specifically request the combining of:

- Groups XXVI and XXIX (claims 11 and 13-16) and

- Groups B, C, and H (claims 11 and 13-16).

Nonetheless, to be fully responsive, Applicants provisionally elect the subject matter of Group XXVI and group H, claims 11, 13, and 16, with traverse.

Should the Examiner combine the groups as respectfully requested, Applicants would elect the combined groups of XXVI and XXIX as well as groups B, C, and H, thereby adding claims 14 and 15, for a total selection of claims 11 and 13-16. In either case, the right to pursue non-elected subject matter in one or more divisional applications is expressly reserved.

Please grant any extensions of time required to enter this paper and charge any additional required fees to Deposit Account No. 06-0916.

Respectfully submitted,

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Dated: August 14, 2008

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